RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/978,318D_

Source: _1Fw/16_

Date Processed by STIC: _9/29/05_

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IFW16

RAW SEQUENCE LISTING   DATE: 09/29/2005
PATENT APPLICATION: US/09/978,318D   TIME: 09:37:44

Input Set : **D:\UTSC671US.txt**
Output Set: **N:\CRF4\09292005\I978318D.raw**

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 3 <110> APPLICANT: ALDAZ, MARCELO C.
 4        BEDNAREK, ANDRZEJ
 6 <120> TITLE OF INVENTION: WWOX: A PUTATIVE TUMOR SUPPRESSOR GENE MUTATED IN
 7        MULTIPLE CANCERS
 9 <130> FILE REFERENCE: UTSC:671US
11 <140> CURRENT APPLICATION NUMBER: 09/978,318D
12 <141> CURRENT FILING DATE: 2001-10-15
14 <150> PRIOR APPLICATION NUMBER: 60/240,277
15 <151> PRIOR FILING DATE: 2000-10-13
17 <160> NUMBER OF SEQ ID NOS: 70
19 <170> SOFTWARE: PatentIn Ver. 2.1
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23 <211> LENGTH: 2264
24 <212> TYPE: DNA
25 <213> ORGANISM: Human
27 <400> SEQUENCE: 1
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29 tgagttcctg agcgagtgga cccggcagcg ggcgataggg gggccaggtg cctccacagt 120
30 cagccatggc agcgctgcgc tacgcggggc tggacgacac ggacagtgag gacgagctgc 180
31 ctccgggctg ggaggagaga accaccaagg acggctgggt ttactacgcc aatcacaccg 240
32 aggagaagac tcagtgggaa catccaaaaa ctggaaaaag aaaacgagtg gcaggagatt 300
33 tgccatacgg atgggaacaa gaaactgatg agaacggaca agtgtttttt gttgaccata 360
34 taaataaaag aaccacctac ttggacccaa gactggcgtt tactgtggat gataatccga 420
35 ccaagccaac cacccggcaa agatacgacg gcagcaccac tgccatggaa attctccagg 480
36 gccgggattt cactggcaaa gtggttgtgg tcactggagc taattcagga atagggttcg 540
37 aaaccgccaa gtcttttgcc ctccatggtg cacatgtgat cttggcctgc aggaacatgg 600
38 caagggcgag tgaagcagtg tcacgcattt tagaagaatg gcataaagcc aaggtagaag 660
39 caatgaccct ggacctcgct ctgctccgta gcgtgcagca ttttgctgaa gcattcaagg 720
40 ccaagaatgt gcctcttcat gtgcttgtgt gcaacgcagc aacttttgct ctaccctgga 780
41 gtctcaccaa agatggcctg gagaccacct ttcaagtgaa tcatctgggg cacttctacc 840
42 ttgtccagct cctccaggat gttttgtgcc gctcagctcc tgcccgtgtc attgtggtct 900
43 cctcagagtc ccatcgattt acagatatta acgactcctt gggaaaactg gacttcagtc 960
44 gcctctctcc aacaaaaaac gactattggg cgatgctggc ttataacagg tccaagctct 1020
45 gcaacatcct cttctccaac gagctgcacc gtcgcctctc cccacgcggg gtcacgtcga 1080
46 acgcagtgca tcctggaaat atgatgtact ccaacattca tcgcagctgg tgggtgtaca 1140
47 cactgctgtt taccttggcg aggcctttca ccaagtccat gcaacaggga ctgccacca 1200
48 ccgtgtactg tgctgctgtc ccagaactgg agggtctggg agggatgtac ttcaacaact 1260
49 gctgccgctg catgccctca ccagaagctc agagcgaaga gacggcccgg accctgtggg 1320
50 cgctcagcga gaggctgatc caagaacggc ttggcagcca gtccggctaa gtggagctca 1380
51 gagcggatgg gcacacacac ccgccctgtg tgtgtcccct cacgcaagtg ccagggctgg 1440
52 gcccCttcca aatgtccctc caacacagat ccgcaagagt aaaggaaata agagcagtca 1500
53 caacagagtg aaaaatctta agtaccaatg ggaagcaggg aattcctggg gtaaagtatc 1560
54 actttctggg gctgggcta ggcataggtc tctttgcttt ctggtggtgg cctgtttgaa 1620
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55 agtaaaaacc tgcttggtgt gtaggttccg tatctccctg gagaagcacc agcaattctc 1680
56 tttcttttac tgttatagaa tagcctgagg tcccctcgtc ccatccagct accaccacgg 1740
57 ccaccactgc agccgggggc tggccttctc ctacttaggg aagaaaaagc aagtgttcac 1800
58 tgctccttgc tgcattgatc caggagataa ttgtttcatt catcctgacc aagactgagc 1860
59 cagcttagca actgctgggg agacaaatct cagaaccttg tcccagccag tgaggatgac 1920
60 agtgacaccc agagggagta gaatacgcag aactaccagg tggcaaagta cttgtcatag 1980
61 actcctttgc taatgctatg caaaaaattc tttagagatt ataacaaatt tttcaaatca 2040
62 ttccttagat accttgaaag gcaggaaggg aagcgtatat acttaagaat acacaggata 2100
63 ttttgggggg cagagaataa aacgttagtt aatccctttg tctgtcaatc acagtctcag 2160
64 ttctcttgct ttcacattgt acttaaacct cctgctgtgc ctcgcatcct atgcttaata 2220
65 aaagaacatg cttgaatatc aaaaaaaaaa aaaaaaaaa aaaa   2264
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69 <211> LENGTH: 414
70 <212> TYPE: PRT
71 <213> ORGANISM: Human
73 <400> SEQUENCE: 2
74 Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu Asp
75 1   5   10   15
77 Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp Val
78   20   25   30
80 Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys
81   35   40   45
83 Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu
84   50   55   60
86 Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn
87 65   70   75   80
89 Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp
90   85   90   95
92 Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr
93   100   105   110
95 Ala Met Glu Ile Leu Gln Gly Arg Asp Phe Thr Gly Lys Val Val Val
96   115   120   125
98 Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe
99   130   135   140
101 Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg
102 145   150   155   160
104 Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys
105   165   170   175
107 Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln His
108   180   185   190
110 Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu Val
111   195   200   205
113 Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly
114   210   215   220
116 Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu Val
117 225   230   235   240
119 Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val Ile
120   245   250   255
122 Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu

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123           260              265              270
125 Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp
126           275              280              285
128 Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser
129      290              295              300
131 Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala
132 305              310              315              320
134 Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp
135              325              330              335
137 Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met
138           340              345              350
140 Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu
141           355              360              365
143 Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro
144      370              375              380
146 Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu
147 385              390              395              400
149 Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly
150              405              410
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 26
154 <212> TYPE: DNA
155 <213> ORGANISM: Homo sapiens
157 <400> SEQUENCE: 3
158 acggtggtgg cagctccctg ttgttg                                26
161 <210> SEQ ID NO: 4
162 <211> LENGTH: 29
163 <212> TYPE: DNA
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 4
167 acggtggtgg cagctccctg ttgcgatgg                             29
170 <210> SEQ ID NO: 5
171 <211> LENGTH: 33
172 <212> TYPE: DNA
173 <213> ORGANISM: Homo sapiens
175 <400> SEQUENCE: 5
176 acggtggtgg cagctccctg ttgacattct tgg                        33
179 <210> SEQ ID NO: 6
180 <211> LENGTH: 32
181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 6
185 acggtggtgg cagctccctg ttgccattct tc                         32
188 <210> SEQ ID NO: 7
189 <211> LENGTH: 30
190 <212> TYPE: DNA
191 <213> ORGANISM: Homo sapiens
193 <400> SEQUENCE: 7
194 acggtggtgg cagctccctg ttgctattcc                            30
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Input Set : D:\UTSC671US.txt
Output Set: N:\CRF4\09292005\I978318D.raw
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197 <210> SEQ ID NO: 8
198 <211> LENGTH: 33
199 <212> TYPE: DNA
200 <213> ORGANISM: Homo sapiens
202 <400> SEQUENCE: 8
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207 <211> LENGTH: 27
208 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 9
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215 <210> SEQ ID NO: 10
216 <211> LENGTH: 19
217 <212> TYPE: DNA
218 <213> ORGANISM: Homo sapiens
220 <400> SEQUENCE: 10
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224 <210> SEQ ID NO: 11
225 <211> LENGTH: 21
226 <212> TYPE: DNA
227 <213> ORGANISM: Homo sapiens
229 <400> SEQUENCE: 11
230 agctccctgt tgcatggact t                                     21
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234 <211> LENGTH: 22
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 12
239 tgagtgctgt ctccatgttt ga                                    22
242 <210> SEQ ID NO: 13
243 <211> LENGTH: 22
244 <212> TYPE: DNA
245 <213> ORGANISM: Homo sapiens
247 <400> SEQUENCE: 13
248 tctgctcccc acctctaagt tg                                    22
251 <210> SEQ ID NO: 14
252 <211> LENGTH: 21
253 <212> TYPE: DNA
254 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 14
257 aggcagtgcg caggcgtgag c                                     21
260 <210> SEQ ID NO: 15
261 <211> LENGTH: 22
262 <212> TYPE: DNA
263 <213> ORGANISM: Homo sapiens
265 <400> SEQUENCE: 15
266 cagccctggc acttgcgtga gg                                    22
269 <210> SEQ ID NO: 16
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PATENT APPLICATION: US/09/978,318D   TIME: 09:37:44

Input Set : D:\UTSC671US.txt
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270 <211> LENGTH: 22
271 <212> TYPE: DNA
272 <213> ORGANISM: Homo sapiens
274 <400> SEQUENCE: 16
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278 <210> SEQ ID NO: 17
279 <211> LENGTH: 23
280 <212> TYPE: DNA
281 <213> ORGANISM: Homo sapiens
283 <400> SEQUENCE: 17
284 gagttcctga gcgagtggac ccg                                   23
287 <210> SEQ ID NO: 18
288 <211> LENGTH: 30
289 <212> TYPE: DNA
290 <213> ORGANISM: Homo sapiens
292 <400> SEQUENCE: 18
293 tagtttttat tattattagt ttttattatt                            30
296 <210> SEQ ID NO: 19
297 <211> LENGTH: 22
298 <212> TYPE: DNA
299 <213> ORGANISM: Homo sapiens
301 <400> SEQUENCE: 19
302 aatactacat cctaaacaac aa                                    22
305 <210> SEQ ID NO: 20
306 <211> LENGTH: 30
307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
310 <400> SEQUENCE: 20
311 agtttttatt attatgagtt tttattaaat                            30
314 <210> SEQ ID NO: 21
315 <211> LENGTH: 20
316 <212> TYPE: DNA
317 <213> ORGANISM: Homo sapiens
319 <220> FEATURE:
320 <221> NAME/KEY: modified_base
321 <222> LOCATION: (3)..(5)
322 <223> OTHER INFORMATION: R = A OR G
324 <400> SEQUENCE: 21
325 ccrcrcaata ctacatccta                                       20
328 <210> SEQ ID NO: 22
329 <211> LENGTH: 20
330 <212> TYPE: DNA
331 <213> ORGANISM: Homo sapiens
333 <220> FEATURE:
334 <221> NAME/KEY: modified_base
335 <222> LOCATION: (11)
336 <223> OTHER INFORMATION: Y = C OR T/U
338 <400> SEQUENCE: 22
339 gggatgaggt ygttttgttt                                       20
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VERIFICATION SUMMARY   DATE: 09/29/2005
PATENT APPLICATION: **US/09/978,318D**   TIME: 09:37:45

Input Set : **D:\UTSC671US.txt**
Output Set: **N:\CRF4\09292005\I978318D.raw**

L:678 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32